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RESPONSE UNDER 37 CFR §1.111
Examining Group 1638
Patent Application
Docket No. CIB-T100XC1
Serial No. 09/685,403

September 3, 2003

Amy Nguyen
Amy Nguyen, Legal Assistant



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Examiner : David H. Kruse
Art Unit : 1638
Applicants : Peter R. Beetham, Patricia L. Avissar, Keith A. Walker, Richard A. Metz
Serial No. : 09/685,403
Filed : October 10, 2000
Confirm. No. : 4644
For : Non-Transgenic Herbicide Resistant Plant

Drawing Review Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

SUBMISSION OF FORMAL DRAWINGS

Sir:

Submitted herewith please find 14 sheets of formal drawings (Figs. 1-7). The Examiner is respectfully requested to acknowledge receipt of these formal drawings.

The submitted drawings are now all on the same size paper and are believed to obviate the informalities indicated on Form PTO-948 attached to the Office Action mailed June 3, 2003.

Respectfully submitted,

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JS/an

Attachments: 14 sheets of formal drawings



DNA sequence:

cccttcacgtcctttttagaaccacattatctttcttagggcccaattgaaaaccacattttctttcacctaacc
ccaaagccttgacacatgttgacgtgaacaccaaactaacacgtgtcatactgccagtggttatgataaatgctcatacc
ataccagagtcataagatgttttggttggtgaaagatttgacggatgccttcttctcatttctcaccacacccctccaaa
cccaacaaaatgtttatattagcaaacgcccgaagtgtaaacgaaagttataaatttcatttctgtgatcttacgta
attggaggagaatcaaaattttcaatccccattcttcgattgcttcaattgaagtttctccg

[transit peptide start]

ATGGCGCAAGTTAGCAGAATCTGCAATGGTGTGCAGAACCCATCTCTTATCTCCAATCTCTCGAAATCCAGTCAACGCA
AATCTCCCTTATCGGTTTCTCTGAAGACGCAGCAGCATCCACGAGCTTATCCGATTTCTGTCGTGCTGGGGATTGAAGAA
GAGTGGGATGACGTTAATTGGCTCTGAGCTTCGTCCTCTTAAGGTCATGTCTTCTGTTTCCACGGCGGAG

[mature peptide starts]

AAAGCGTCCGAGATTGTAACCTCAACCCATTAGAGAAATCTCCGCTCTTATTAAGCTTCTCTGGCTCCAAGTCTCTATCAA
ATCGGATCCTGCTTCTCGCTGCTCTGCTGAGGTATATATCACTTCGTTTCGTCCTTCTCTGTAATCTGAACCTTAGATT
ATAAAGATTGATACTTTACCATTTTGTCTGTGGTTTTATAGGGAACAACCTGTAGTGGACAACCTGTTGAATAGCGATGAC
ATCAATTACATGCTTGATGCGTTGAAGAGATTGGGACTTAATGTGGAACTGACAGTGAAAATAATCGTGTCTGTAGTTG
AAGGATGTGGCGGGATATTCCAGCTTCCATAGATTCAAAGAGTGATATCGAACTTTACCTCGGTAATGCAGGAACAGC
AATGCGTCCCACTTACCCTGCGGTCACTGCTGCAGGTGGAACGCAAGGTAGATTGAAGGAGTTGATGCTTCTTGGTAT
TTGATGTTTAAGGAATGGAGCTTTTGTGATGCTTTATGATCCATTTATTCAGTTATGTGCTTGATGGGTGCCTCGT
ATGAGAGAAAGACCTATAGGGGATTGGTGTGGTCTTAAGCAGCTTGGTGTGATGTTGAATGTACTCTTGGAACTA
ACTGCCCTCTGTTCTGTCAACGCTAATGGTGGCCTTCCCGGTGGAAGGTTAGATCTTGCAAATGGCATGTGAATAT
GTAATCTCGTTCCTTACTCTATGAACACTTGCAGAAATGTGTGTTTATCATAGCCTTAGCTTGACAAGATTTCACTTTT
TAATCTACTCTCAACGGATGGATCCTAAATAGAAATCGGATTTGGTGATTGGTTTTCTGTTCTCGATTACCGTTTTCTGTT
GTATGATTTCTTGATTAACAATTAGGAGACATGTTATGCATTTGCAGGTGAAGCTTCTGGATCAATTAGTAGTCAGTA
CTTGACTGCTCTGCTCATGTCTGCTCCCTTAGCTCTTGGAGACGTCGAGATTGAGATTGTGATAAATTAATTTCTGTT
CCATATGTTGAAATGACATTGAAGTTGATGGAACGTTTTCGGGGTTAGTGTGAGCATAGTGATAGCTGGGATCGTTTCT
TTGTCAAGGGCGGGCAAAAATACAAGTAGGAGTTATTCTTTTCTTCTTTTCTGAAATCACATCCCTTAGCTTGACAAT
ATAATGACTAAAAGGTGAATGATTCAAGTCTCCGGGTAATGCGTATGTAGAAGGTGATGCTTCTAGTGATGTTATTTC
TTGGCTGGTGTGCCATTACCGGTGAACTGTACAGTCGAAGGTTGTGGAACCTACCAGCTTGACAGTAATATTTGTAC
ACTGAATCATCGACGAGGCTGTTAAGTTTATAGTGAAATTCGTCTAGGTCAAAGTTTCATCTTTTGACAAGTTGTATAT
AACATATTCGCAAGATTCTAAGCTCAATTTTTGTGATGAATCTCTAGGGAGATGTAAAATTCGCCGAGGTCCTTGAGAA
AATGGGATGTAAAGTGTCTGGACAGAGAACAGTGTGACTGTGACAGGACCACCTAGAGATGCTTTTGAATGAGACAC
TTGCGGGCTATTGATGTCAACATGAACAAAATGCCTGATGTAGCCATGACCCTTGCCGTCGTTGCTCTCTTTGCTGACG
GTCCAACCACCATTAGAGATGGTAAGTAAAAGCTCTCTCTTATAATTAAGGTTTCTCAATATTGATGATCACTTAATT
CTGTTTGGTTAATATAGTGGCTAGCTGGAGAGTAAAGGAGACAGAAAGGATGATTGCCATTTGCACAGAGCTTAGAAAA
GTAAGAGATTCTTATCTCTCTCTTTCTGTCTCTTGACAGTGCTCATTCTAAGTAATTAGCTCATAAATTTGTGTGTTG
TGTTCACTGGGAGCTACAGTGAAGAAGGTTCAAGATTATTGTGTGATAACTCCGCCCAAAAAGGTGAAAACGGCAGAG
ATTGATACATATGATGATCATAGAAATGGCAATGGCATTCTCTCTTGCAGCTGTGCTGATGTTCCAATCACCATCAACG
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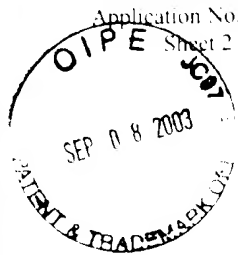
FIG. 1A

Title: Non-Transgenic Herbicide Resistant Plant

Inventor(s): Beetham *et al.*

Application No.: 09/685,403

Sheet 2 of 14



Protein sequence:

MAQVSRICNGVQNPSLISNLSKSSQRKSPLSVSLKTQQHPRAYPISSSWGLKKSGMTLIGSELRLPKVMSSVSTAE
KASEIVLQPIREISGLIKLPGSKSLNRIILLALSEGTTVDNLLNSDDINYMLDALKRLGLNVETDSENNRAVV
EGCGGIFPASIDSKSDIELYLGNAGTAMRPLTAAVTAAGGNASYVLDGVPRMRERPIGDLVVGLKQLGADVECTLG
TNCPPVRVNANGGLPGGKVKLSGSISSQYLTAALLMSAPLALGDVEIEIVDKLISVPYVEMTLKLMERFGVSVEHSD
SWDRFFVKGGQKYKSPGNAYVEGDASSACYFLAGAAITGETVTVEGCGTTSLQGDVKFAEVLEKMGCKVSWTENS
TVTGPPRDAFGMRHLRAIDVNMNKM~~P~~DVAMTLAVVALFADGPTTIRDVASWRVKETERMIAICTELRKL~~G~~ATVEEG
SDYCVITPPKKVKTAEIDTYDDHRMAMAFSLAACADVPIITINDSGCTRKTFPDYFQVLERITKH

FIG. 1B



Arabidopsis thaliana wild type sequence:

Position	173	174	175	176	177	178	179	180	181	182	183
	L	G	N	A	G	T	A	M	R	P	L
	CTC	GGT	AAT	GCA	GGA	ACA	GCA	ATG	CGT	CCA	CTT

Arabidopsis thaliana mutant sequences:

Name											
A ₁₇₇	CTC	GGT	AAT	GCA	GCA	ACA	GCA	ATG	CGT	CCA	CTT
	L	G	N	A	A	T	A	M	R	P	L
I ₁₇₈	CTC	GGT	AAT	GCA	GGA	ATA	GCA	ATG	CGT	CCA	CTT
	L	G	N	A	I	T	A	M	R	P	L
A ₁₇₇ I ₁₇₈	CTC	GGT	AAT	GCA	GCA	ATA	GCA	ATG	CGT	CCA	CTT
	L	G	N	A	A	I	A	M	R	P	L
I ₁₇₈ S ₁₈₂	CTC	GGT	AAT	GCA	GGA	ATA	GCA	ATG	CGT	TCA	CTT
	L	G	N	A	G	I	A	M	R	S	L
A ₁₇₇ S ₁₈₂	CTC	GGT	AAT	GCA	GCA	ACA	GCA	ATG	CGT	TCA	CTT
	L	G	N	A	A	T	A	M	R	S	L
A ₁₇₇ I ₁₇₈ S ₁₈₂	CTC	GGT	AAT	GCA	GCA	ATA	GCA	ATG	CGT	TCA	CTT
	L	G	N	A	A	I	A	M	R	S	L
V ₁₇₈ S ₁₈₂	CTC	GGT	AAT	GCA	GGA	GTA	GCA	ATG	CGT	TCA	CTT
	L	G	N	A	G	V	A	M	R	S	L
L ₁₇₈ S ₁₈₂	CTC	GGT	AAT	GCA	GGA	TTA	GCA	ATG	CGT	TCA	CTT
	L	G	N	A	G	L	A	M	R	S	L
A ₁₇₇ V ₁₇₈	CTC	GGT	AAT	GCA	GCA	GTA	GCA	ATG	CGT	CCA	CTT
	L	G	N	A	A	V	A	M	R	P	L
A ₁₇₇ L ₁₇₈	CTC	GGT	AAT	GCA	GCA	TTA	GCA	ATG	CGT	CCA	CTT
	L	G	N	A	A	L	A	M	R	P	L

FIG. 2

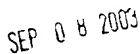

$$\frac{1}{2}$$



Figure 1 displays the DNA sequence alignment of the 5' region of the 28S rRNA gene from various species. The alignment is presented in 10 columns, each representing a different species. The sequences are aligned from position 285 to 568. The species names are listed on the left: (285) A. seq, (286) A. seq, (287) A. seq, (288) A. seq, (289) A. seq, (290) A. seq, (291) A. seq, (292) A. seq, (293) A. seq, (294) A. seq, (295) A. seq, (296) A. seq, (297) A. seq, (298) A. seq, (299) A. seq, (300) A. seq, (301) A. seq, (302) A. seq, (303) A. seq, (304) A. seq, (305) A. seq, (306) A. seq, (307) A. seq, (308) A. seq, (309) A. seq, (310) A. seq, (311) A. seq, (312) A. seq, (313) A. seq, (314) A. seq, (315) A. seq, (316) A. seq, (317) A. seq, (318) A. seq, (319) A. seq, (320) A. seq, (321) A. seq, (322) A. seq, (323) A. seq, (324) A. seq, (325) A. seq, (326) A. seq, (327) A. seq, (328) A. seq, (329) A. seq, (330) A. seq, (331) A. seq, (332) A. seq, (333) A. seq, (334) A. seq, (335) A. seq, (336) A. seq, (337) A. seq, (338) A. seq, (339) A. seq, (340) A. seq, (341) A. seq, (342) A. seq, (343) A. seq, (344) A. seq, (345) A. seq, (346) A. seq, (347) A. seq, (348) A. seq, (349) A. seq, (350) A. seq, (351) A. seq, (352) A. seq, (353) A. seq, (354) A. seq, (355) A. seq, (356) A. seq, (357) A. seq, (358) A. seq, (359) A. seq, (360) A. seq, (361) A. seq, (362) A. seq, (363) A. seq, (364) A. seq, (365) A. seq, (366) A. seq, (367) A. seq, (368) A. seq, (369) A. seq, (370) A. seq, (371) A. seq, (372) A. seq, (373) A. seq, (374) A. seq, (375) A. seq, (376) A. seq, (377) A. seq, (378) A. seq, (379) A. seq, (380) A. seq, (381) A. seq, (382) A. seq, (383) A. seq, (384) A. seq, (385) A. seq, (386) A. seq, (387) A. seq, (388) A. seq, (389) A. seq, (390) A. seq, (391) A. seq, (392) A. seq, (393) A. seq, (394) A. seq, (395) A. seq, (396) A. seq, (397) A. seq, (398) A. seq, (399) A. seq, (400) A. seq, (401) A. seq, (402) A. seq, (403) A. seq, (404) A. seq, (405) A. seq, (406) A. seq, (407) A. seq, (408) A. seq, (409) A. seq, (410) A. seq, (411) A. seq, (412) A. seq, (413) A. seq, (414) A. seq, (415) A. seq, (416) A. seq, (417) A. seq, (418) A. seq, (419) A. seq, (420) A. seq, (421) A. seq, (422) A. seq, (423) A. seq, (424) A. seq, (425) A. seq, (426) A. seq, (427) A. seq, (428) A. seq, (429) A. seq, (430) A. seq, (431) A. seq, (432) A. seq, (433) A. seq, (434) A. seq, (435) A. seq, (436) A. seq, (43

[illegible]

(853) 853
(844) 860
(832) 870
(832) 880
(622) 890
(853) 900
910
920

Section 14

Parameter	1. seq
bnd	a. seq
pea	a. seq
...	s. seq
...	cons

Section 14

(924) 924 CTGGGATCGTTTCTTTGTCAGGGCGGTCAGAAATACAAGTCTCCTGCTTATGCTATGTTAGAAAGGTGATG
(915) 925 CTGGGATCGTTTCTTTGTCAGGGCGGTCAGAAATACAAGTCTCCTGCTTATGCTATGTTAGAAAGGTGATG
(903) 926 CTGGGATCGTTTCTTTGTCAGGGCGGTCAGAAATACAAGTCTCCTGCTTATGCTATGTTAGAAAGGTGATG
(903) 927 CTGGGATCGTTTCTTTGTCAGGGCGGTCAGAAATACAAGTCTCCTGCTTATGCTATGTTAGAAAGGTGATG
(693) 928 CTGGGATCGTTTCTTTGTCAGGGCGGTCAGAAATACAAGTCTCCTGCTTATGCTATGTTAGAAAGGTGATG
(924) 929 CTGGGATCGTTTCTTTGTCAGGGCGGTCAGAAATACAAGTCTCCTGCTTATGCTATGTTAGAAAGGTGATG

Category	Seq
ateq	a.seq
lne	a.seq
peta	a.seq
...	s.seq

Section 15

(995) 995
 (996) 1000
 (974) 1010
 (974) 1020
 (764) 1030
 (995) 1040
 1050
 1065
 Section 16

category	A.seq
base	a.a.seq
protein	aa.seq
	ps.seq
	consus

Section 16

[illegible]

ate. A.seq
br a.seq
patri a.seq
ps.seq
ensus



Section 17

[illegible]

atel
buc
petar

Section 18

[illegible]

ate
but
pe a.

Section 19

[illegible]

ated, and

Section 20

[illegible]

atc
by
p. 10

	(1563)	1563	1572
ate;	a.seq (1554)	ATTA	CTTA
trp	a.seq (1542)	TATA	CTTA
petA	a.seq (1542)	CTAA	CTGA
g	s.seq (1332)	TTAA	-----
	consus (1563)	AAAGCATTTAA	



Section 5

(297) 297
 (290) LKLMERFGVSAEHSBSWDRFFVKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTIVVEGCGTTSLOQGDVKFA
 (286) LKLMERFGVSAEHSBSWDRFFVKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTIVVEGCGTTSLOQGDVKFA
 (286) LKLMERFGVSAEHSBSWDRFFVKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTIVVEGCGTTSLOQGDVKFA
 (214) LKLMERFGVSAEHSBSWDRFFVKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTIVVEGCGTTSLOQGDVKFA
 (297) LKLMERFGVSAEHSBSWDRFFVKGGQKYKSPGNAYVEGDASSASYFLAGAAITGGTIVVEGCGTTSLOQGDVKFA

Section 6

(371) 371
 (364) EVLEKMGCKVSWTENSVTVTGPPRDVAFGRKHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE
 (360) EVLEKMGCKVSWTENSVTVTGPPRDVAFGRKHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE
 (360) EVLEKMGCKVSWTENSVTVTGPPRDVAFGRKHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE
 (288) EVLEKMGCKVSWTENSVTVTGPPRDVAFGRKHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE
 (371) EVLEKMGCKVSWTENSVTVTGPPRDVAFGRKHLRAIDVNMNKMPPDVAMTLAVVALFADGPTTIRDVASWRVKETE

Section 7

(445) 445
 (438) RMIAICTELRKLGLATVEEGSDYCIITPPEKLNVTETIDYDDHRMAMAFSLAACADVPVTINDPGCTRKTFFPDYF
 (434) RMIAICTELRKLGLATVEEGSDYCIITPPEKLNVTETIDYDDHRMAMAFSLAACADVPVTINDPGCTRKTFFPDYF
 (434) RMIAICTELRKLGLATVEEGSDYCIITPPEKLNVTETIDYDDHRMAMAFSLAACADVPVTINDPGCTRKTFFPDYF
 (362) RMIAICTELRKLGLATVEEGSDYCIITPPEKLNVTETIDYDDHRMAMAFSLAACADVPVTINDPGCTRKTFFPDYF
 (445) RMIAICTELRKLGLATVEEGSDYCIITPPEKLNVTETIDYDDHRMAMAFSLAACADVPVTINDPGCTRKTFFPDYF

Section 8

(519) 519
 (512) QVLESITKH
 (508) QVLESITKH
 (508) QVLESITKH
 (436) QVLESITKH
 (519) QVLESITKH



<u>Oligo Name</u>	<u>Oligo Sequence (5'→3')</u>
ATEPS-A ₁₇₇	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAGTGGACGCATTGCTGTT GCT GCATTACCGAG
ATEPS-AI	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAGTGGACGCATTGCT TATTGCT GCATTACCGAG
ATEPS-IS	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAG TGAAC GCATTGCT TATT CCTGCATTACCGAG
ATEPS-AS	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAG TGAAC GCATTGCTGTT GCT GCATTACCGAG
ATEPS-AIS	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAG TGAAC GCATTGCT TATTGCT GCATTACCGAG
ATEPS-I ₁₇₇	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAGTGGACGCATTGCTGTT TATT GCATTACCGAG
ATEPS-VS	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAG TGAAC GCATTGCT TACT CCTGCATTACCGAG
ATEPS-LS	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAG TGAAC GCATTGCT TAAT CCTGCATTACCGAG
ATEPS-AV	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAGTGGACGCATTGCT TACTGCT GCATTACCGAG
ATEPS-AL	CGTTTCCAC <u>CTGCAG</u> CAGTGACCGCAGCGGTAAGTGGACGCATTGCT TAATGCT GCATTACCGAG

FIG. 5

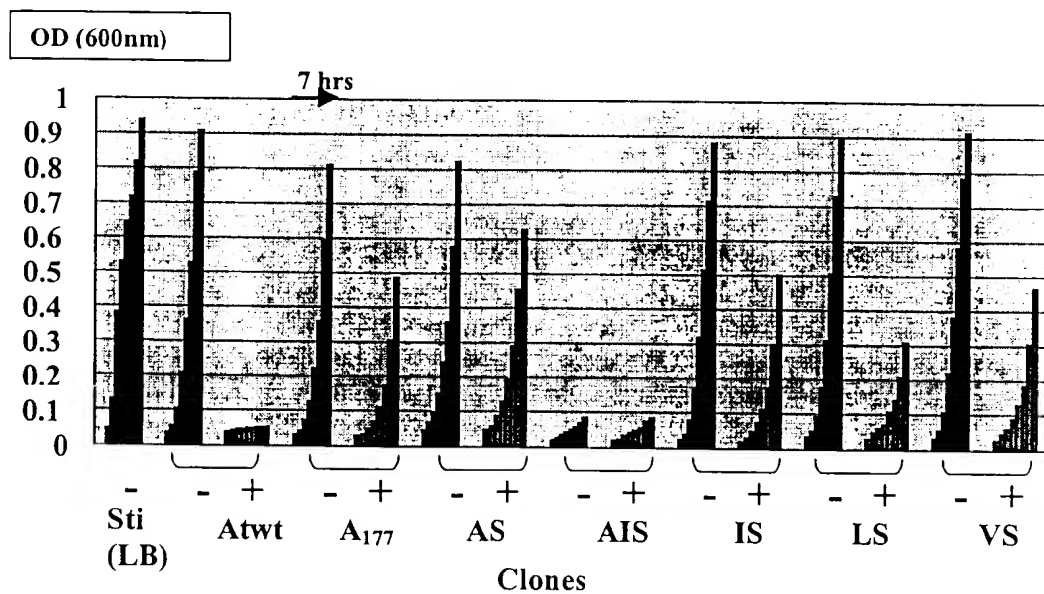


FIG. 6

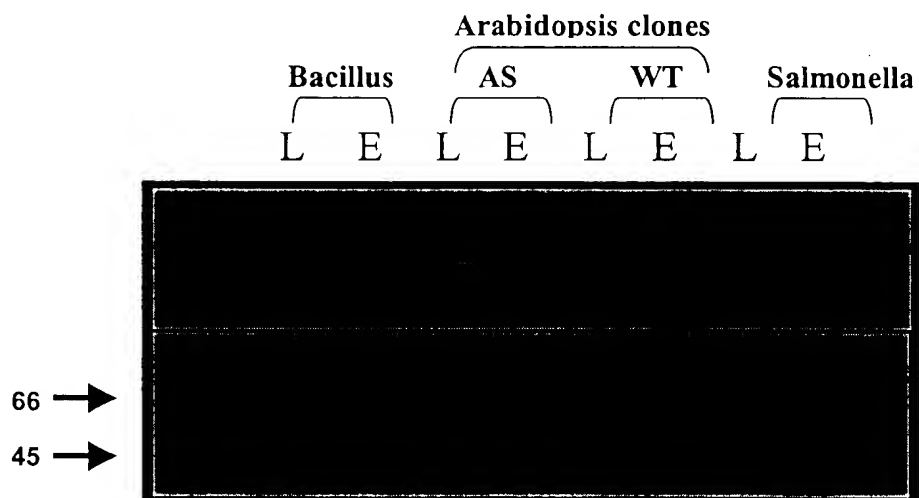


FIG. 7